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RAW SEQUENCE LISTING   DATE: 07/26/2001
PATENT APPLICATION: US/09/775,879   TIME: 09:39:18

Input Set : **A:\22250003seqlist.txt**
Output Set: **N:\CRF3\07262001\I775879.raw**

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 3 <110> APPLICANT: Choe, Sunghwa
 4         Feldmann, Kenneth A
 6 <120> TITLE OF INVENTION: Dwf7 MUTANTS
 8 <130> FILE REFERENCE: 2225-0003
10 <140> CURRENT APPLICATION NUMBER: 09/775,879
11 <141> CURRENT FILING DATE: 2001-02-02
13 <150> PRIOR APPLICATION NUMBER: 60/179,901
14 <151> PRIOR FILING DATE: 2000-02-02
16 <160> NUMBER OF SEQ ID NOS: 25
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 25
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_FF
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33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
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43 <211> LENGTH: 19
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_1F
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51 gcgcaatctt ctttcgttt                                             19
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55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_1R
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66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
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70  <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_2F
72  <400> SEQUENCE: 5
73  gatgcacaga gagcttcatg ac                                              22
75  <210> SEQ ID NO: 6
76  <211> LENGTH: 22
77  <212> TYPE: DNA
78  <213> ORGANISM: Artificial Sequence
80  <220> FEATURE:
81  <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_2R
83  <400> SEQUENCE: 6
84  ccggcaaatg gagagagtgt at                                              22
86  <210> SEQ ID NO: 7
87  <211> LENGTH: 21
88  <212> TYPE: DNA
89  <213> ORGANISM: Artificial Sequence
91  <220> FEATURE:
92  <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_3F
94  <400> SEQUENCE: 7
95  cacccatcat atctacaaca a                                               21
97  <210> SEQ ID NO: 8
98  <211> LENGTH: 22
99  <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer S5D_4F
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106 catcttttgc cggcgaatct at                                              22
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109 <211> LENGTH: 32
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer D7-5-1
116 <400> SEQUENCE: 9
117 gtagaagcac cagaggaaac cggagatgaa gt                                   32
119 <210> SEQ ID NO: 10
120 <211> LENGTH: 26
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer D7-5-2
127 <400> SEQUENCE: 10
128 aagtatagta gggttccggc gaggta                                         26
130 <210> SEQ ID NO: 11
131 <211> LENGTH: 26
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer D7-5-3
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138 <400> SEQUENCE: 11
139 atagattcgc cggcaaaaga tgactc                                    26
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142 <211> LENGTH: 32
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer D7-3-1
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153 <211> LENGTH: 35
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer D7-3-2
160 <400> SEQUENCE: 13
161 catacgatac accacacgac atacaagcat aacta                          35
163 <210> SEQ ID NO: 14
164 <211> LENGTH: 28
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer D7-3-3
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174 <210> SEQ ID NO: 15
175 <211> LENGTH: 364
176 <212> TYPE: PRT
177 <213> ORGANISM: delta-7 sterol C-5 desaturase (Candida glabrata)
179 <400> SEQUENCE: 15
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181  1               5                  10                  15
183 Tyr Ala Lys Ile Ala Pro Val Glu Leu Gln Arg Gly Ile Asp Asp Ser
184             20                  25                  30
186 Leu Val Asn Ala Leu Ser Leu Asn Lys Ile Val Ser Asn Ser Thr Leu
187             35                  40                  45
189 Leu His Glu Thr Leu Ser Ile Thr Asn Ser Leu Lys Arg Val Asn Lys
190     50                  55                  60
192 Asp Val Tyr Gly Leu Thr Pro Phe Leu Phe Asp Phe Thr Glu Lys Thr
193 65                  70                  75                  80
195 Tyr Ala Ser Leu Leu Pro Arg Asn Asn Leu Ile Arg Glu Phe Phe Ser
196                 85                  90                  95
198 Leu Trp Ala Val Val Thr Val Phe Gly Leu Leu Leu Tyr Leu Ile Thr
199             100                 105                 110
201 Ala Ser Leu Ser Tyr Val Phe Val Phe Asp Arg Thr Ile Phe Asn His
202             115                 120                 125
204 Pro Lys Tyr Leu Lys Asn Gln Met Tyr Leu Glu Ile Lys Leu Ala Val
205         130                 135                 140
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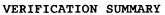
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207 Ser Ala Ile Pro Thr Met Ser Leu Leu Thr Val Pro Trp Phe Met Leu
208 145             150             155                 160
210 Glu Leu Asn Gly Tyr Ser Lys Leu Tyr Tyr Asp Val Asp Trp Glu His
211             165             170             175
213 His Gly Leu Arg Lys Leu Leu Ile Glu Tyr Ala Thr Phe Ile Phe Phe
214             180             185             190
216 Thr Asp Cys Gly Ile Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg
217         195             200             205
219 Val Tyr Lys Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr
220     210             215             220
222 Pro Phe Ala Ser His Ala Phe His Pro Val Asp Gly Tyr Phe Gln Ser
223 225             230             235                 240
225 Leu Ser Tyr His Ile Tyr Pro Met Ile Leu Pro Leu His Lys Ile Ser
226             245             250             255
228 Tyr Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Ser Val Met Ile His
229             260             265             270
231 Asp Gly Gln His Met Ser Asn Asn Pro Val Val Asn Gly Thr Ala Cys
232         275             280             285
234 His Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr
235     290             295             300
237 Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Glu Asp Ser
238 305             310             315                 320
240 Leu Phe Asp Pro Lys Leu Lys Met Asp Lys Lys Val Leu Glu Lys Gln
241             325             330             335
243 Ala Arg Glu Thr Ala Ala Tyr Ile Gln Glu Val Glu Gly Asp Asp Thr
244             340             345             350
246 Asp Arg Val Tyr Asn Thr Asp Lys Lys Lys Thr Asn
247         355             360
250 <210> SEQ ID NO: 16
251 <211> LENGTH: 365
252 <212> TYPE: PRT
253 <213> ORGANISM: delta-7 sterol C-5 desaturase (Saccharomyces cerevisiae)
255 <400> SEQUENCE: 16
256 Met Asp Leu Val Leu Glu Val Ala Asp His Tyr Val Leu Asp Asp Leu
257 1             5             10             15
259 Tyr Ala Lys Val Leu Pro Ala Ser Leu Ala Ala Asn Ile Pro Val Lys
260             20             25             30
262 Trp Gln Lys Leu Leu Gly Leu Asn Ser Gly Phe Ser Asn Ser Thr Ile
263         35             40             45
265 Leu Gln Glu Thr Leu Asn Ser Lys Asn Ala Val Lys Glu Cys Arg Arg
266     50             55             60
268 Phe Tyr Gly Gln Val Pro Phe Leu Phe Asp Met Ser Thr Thr Ser Phe
269 65             70             75                 80
271 Ala Ser Leu Leu Pro Arg Ser Ser Ile Leu Arg Glu Phe Leu Ser Leu
272             85             90             95
274 Trp Val Ile Val Thr Ile Phe Gly Leu Leu Leu Tyr Leu Phe Thr Ala
275             100             105             110
277 Ser Leu Ser Tyr Val Phe Val Phe Asp Lys Ser Ile Phe Asn His Pro
278             115             120             125
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280 Arg Tyr Leu Lys Asn Gln Met Ala Met Glu Ile Lys Leu Ala Val Ser
281    130              135              140
283 Ala Ile Pro Trp Met Ser Met Leu Thr Val Pro Trp Phe Val Met Glu
284 145              150              155              160
286 Leu Asn Gly His Ser Lys Leu Tyr Met Lys Ile Asp Tyr Glu Asn His
287              165              170              175
289 Gly Val Arg Lys Leu Ile Ile Glu Tyr Phe Thr Phe Ile Phe Phe Thr
290              180              185              190
292 Asp Cys Gly Val Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg Val
293     '  195              200              205
295 Tyr Arg Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro
296     210              215              220
298 Phe Ala Ser His Ser Phe His Pro Val Asp Gly Phe Leu Gln Ser Ile
299 225              230              235              240
301 Ser Tyr His Ile Tyr Pro Leu Ile Leu Pro Leu His Lys Val Ser Tyr
302              245              250              255
304 Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Thr Val Met Ile His Asp
305              260              265              270
307 Gly Gln Tyr Leu Ser Asn Asn Pro Ala Val Asn Gly Thr Ala Cys His
308              275              280              285
310 Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr Thr
311     290              295              300
313 Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Asp Asp Ser Leu
314 305              310              315              320
316 Phe Asp Pro Lys Leu Arg Asp Ala Lys Glu Thr Trp Asp Ala Gln Val
317              325              330              335
319 Lys Glu Val Glu His Phe Ile Lys Glu Val Glu Gly Asp Asp Asn Asp
320              340              345              350
322 Arg Ile Tyr Glu Asn Asp Pro Asn Thr Lys Lys Asn Asn
323              355              360              365
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326 <210> SEQ ID NO: 17
327 <211> LENGTH: 329
328 <212> TYPE: PRT
329 <213> ORGANISM: delta-7 sterol C-5 desaturase (Schizosaccharomyces pombe)
331 <400> SEQUENCE: 17

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332 Met Asp Val Val Leu Gln Tyr Ala Asp Lys Tyr Val Phe Asp Thr Phe
333    1              5              10              15
335 Tyr Gly Lys Ile Ala Glu Ser Phe Asp Ser Ser Ser Phe Ala Asn
336              20              25              30
338 Thr Ala Val Asn Ser Thr Thr Leu Gly Leu Ala Glu Lys Val Asn Phe
339              35              40              45
341 Ala Ile Thr Ser Gly Leu Leu Asp Arg Asn Asn Val Trp Arg Gln Phe
342     50              55              60
344 Thr Ser Leu Phe Leu Ile Thr Trp Ile Met Gly Thr Leu Ser Tyr Phe
345 65              70              75              80
347 Leu Ser Ala Ser Phe Ala Tyr Tyr Val Tyr Phe Asp Arg Glu Glu Ala
348              85              90              95
350 Arg Arg His Pro Lys Phe Leu Lys Asn Gln Glu His Leu Glu Leu Met
351              100              105              110
```

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